

CLAIMS

1. A method of analyzing a protein, comprising:
binding a marker to a particular kind of amino acid residue having an unmodified side chain among the particular kinds of amino acid residues constituting the protein;
5 cleaving said protein at a predetermined site and obtaining peptide fragments;
measuring the molecular weights of said peptide fragments; and
determining the presence or absence of said marker
10 bound to the particular kind of amino acid residue in said peptide fragments containing said particular amino acid residue and determining the presence or absence of said side chain modification or the kinds of the modifying groups, by comparing the molecular weight of said peptide fragment
15 calculated from the molecular weights of the amino acid residues constituting said peptide fragment with the molecular weights of the peptide fragments measured in said measuring the molecular weights.
2. The method of analyzing a protein according to Claim 1, wherein said determining the presence or absence of marker bound, the presence or absence of side chain modification, and the kinds of the modifying groups includes
5 a comparing the difference obtained by subtracting by the molecular weight of said peptide fragment calculated from

the molecular weights of the amino acid residues constituting said peptide fragment from the molecular weights of said peptide fragments measured in said measuring
10 the molecular weights with the increase in molecular weight when said marker is bound, and comparing said difference with the molecular weight of said side chain that can modify the particular kind of amino acid residue.

3. The method of analyzing a protein according to Claim 1 or 2,

wherein said obtaining the peptide fragments include treating said protein having said marker bound, with a
5 protease, and

said marker eliminates the sensitivity of said particular kind of amino acid residue to said protease treatment.

4. The method of analyzing a protein according to any one of Claims 1 to 3,

wherein said obtaining the peptide fragments includes obtaining at least one of the peptide fragments containing
5 said particular kind of a single amino acid residue.

5. The method of analyzing a protein according to any one of Claims 1 to 4,

wherein said measuring the molecular weights of the peptide fragments include measuring the mass numbers of said

5 peptide fragments by mass spectrometry.

6. The method of analyzing a protein according to any one of Claims 1 to 5,

wherein said determining the presence or absence of side chain modification or the kinds of the modifying groups
5 includes determining the number of methylation, acetylation, or ubiquitylation of the lysine residues in the peptide fragments or the presence or absence of phosphorylation on the serine or threonine residues in said peptide fragments.

7. The method of analyzing a protein, according to any one of Claims 1 to 6,

wherein said binding a marker includes N-acylating the lysine residues in said protein.

8. The method of analyzing a protein according to any one of Claims 1 to 6,

wherein said binding a marker includes succinylating said particular kind of amino acid residue.

9. The method of analyzing a protein according to any one of Claims 1 to 8,

wherein said obtaining the peptide fragments includes digesting said protein having said marker bound with
5 trypsin.

10. The method of analyzing a protein, according to any one of Claims 1 to 9,
wherein said protein is histone.